



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stojiljkovic, Igor
So, Magdalene
Hwa, Vivian
Heffron, Fred
Nassif, Xavier

(ii) TITLE OF INVENTION: Novel Bacterial Hemoglobin Receptor
Genes and Uses

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
(B) STREET: 300 South Wacker Drive, 32nd Floor
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/537,361
(B) FILING DATE: 02-OCT-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Noonan, Kevin E
(B) REGISTRATION NUMBER: 35,303
(C) REFERENCE/DOCKET NUMBER: 94,784-A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-913-0001
(B) TELEFAX: 312-913-0002

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 471..2848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAACTAGTG GATCCAATTT GGGCGCGCGC TTTTTGTTCA AACACGCCA AAAACTCGAT 60
TACAACGGCG AACACGGCGC GCGCCACCTC GCTCCGCATC CCGACGGGCC GCGGCAAACA 120
CTGGCGCGCC TTCGTCGAGC ATCTTGAACG CTTTGAACCT GACTCCGAA GCCGAAGCGG 180
AAGCCATTCA AGGCGCGCGC GAAGCCTTG CATTCTACAA AGTCGTGTTG CGCGAAACCT 240
TCGGCTTGGC AGCCGATGCC GAAGCCCCCG AAGGTATGAT GCCGCACAGG CACTAAAAAA 300
TAATCGAACCC AAATAAACAA GGTCTCGGCA TAGCTGTTG CAGGGACCTT TAATTACACG 360
GCGCGGCTTT GTTTACATGG ATTACTGTCT TATTAAATAT TAATGATTAT CATAAAATCT 420
ATTATTCGCT AACCGATGGA TGAACAATCC ATACATCTT AGTTGATAAT ATG AAA 476
Met Lys
1
CCA TTA CAA ATG CTC CCT ATC GCC GCG CTG GTC GGC AGT ATT TTC GGC 524
Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile Phe Gly
5 10 15
AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA CCC GTT 572
Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr Pro Val
20 25 30
AAG GCA GAG GTA AAA GCA GTG CGC GGT AAA GGC CAG CGC AAT GCG CCT 620
Lys Ala Glu Val Lys Ala Val Arg Gly Lys Gly Gln Arg Asn Ala Pro
35 40 45 50
GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA ATG ATA 668
Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu Met Ile
55 60 65
CGC GAC AAC AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC TTG AGC 716
Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly Leu Ser
70 75 80
GAC AGC GGC CGC CAT CAA AAA GGC TTT GCT GTT CGC GGC GTG GAA GGC 764
Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val Glu Gly
85 90 95
AAC CGT GTC GGC GTG AGC ATA GAC GGC GTA AAC CTG CCT GAT TCC GAA 812
Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp Ser Glu
100 105 110
GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG CGT CTG 860
Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser Arg Leu
115 120 125 130
TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC ATC GTA AAA GGG GCG 908
Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys Gly Ala
135 140 145
GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG AAT TAC 956
Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val Asn Tyr
150 155 160

B
Cont

CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG TTC GGC Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln Phe Gly 165 170 175	1004
GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG ACA AAT Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp Thr Asn 180 185 190	1052
ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT TTG CTG Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala Leu Leu 195 200 205 210	1100
TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAG CGT GGT Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys Arg Gly 215 220 225	1148
TAT CCG GTA GAG GGT GCT GGT AGC GGA GCG AAT ATC CGT GGT TCT GCG Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly Ser Ala 230 235 240	1196
CGC GGT ATT CCT GAT CCG TCC CAA CAC AAA TAC CAC AGC TTC TTG GGT Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe Leu Gly 245 250 255	1244
AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA TCG CTC Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala Ser Leu 260 265 270	1292
AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC AAC CTG Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr Asn Leu 275 280 285 290	1340
CTT GCT TCT TAT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG CGT AAC Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg Arg Asn 295 300 305	1388
ACC AAC CTC TTT TAC GAA TGG ACG CCG GAA TCC GAC CGG TTG TCT ATG Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu Ser Met 310 315 320	1436
<i>B</i> <i>cont</i>	
GTA AAA GCG GAT GTC GAT TAT CAA AAA ACC AAA GTA TCT GCG GTC AAC Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala Val Asn 325 330 335	1484
TAC AAA GGT TCG TTC CCG ATA GAG GAT TCT TCC ACC TTG ACA CGT AAC Tyr Lys Gly Ser Phe Pro Ile Glu Asp Ser Ser Thr Leu Thr Arg Asn 340 345 350	1532
TAC AAT CAA AAG GAC TTG GAT GAA ATC TAC AAC CGC AGT ATG GAT ACC Tyr Asn Gln Lys Asp Leu Asp Glu Ile Tyr Asn Arg Ser Met Asp Thr 355 360 365 370	1580
CGC TTC AAA CGC ATT ACC CTG CGT TTG GAC AGC CAT CCG TTG CAA CTC Arg Phe Lys Arg Ile Thr Leu Arg Leu Asp Ser His Pro Leu Gln Leu 375 380 385	1628
GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACT TTC GCC AGC CGC CGT Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser Arg Arg	1676

390	395	400	
GAT TTT GAA AAC CTA AAC CGC GAC GAT TAT TAC TTC AGC GGC CGT GTT Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg Val 405 410 415			1724
GTT CGA ACC ACC AGC AGT ATC CAG CAT CCG GTG AAA ACC ACC AAC TAC Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr 420 425 430			1772
GGT TTC TCA CTG TCT GAC CAA ATT CAA TGG AAC GAC GTG TTC AGT AGC Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser 435 440 445 450			1820
CGC GCA GGT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG GAA TTG Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu 455 460 465			1868
AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAC ACT Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr 470 475 480			1916
TAT AAA GGC TGG AGC GGT TTT GTC GGC TTG GCG GCG CAA CTG AAT CAG Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln 485 490 495			1964
GCT TGG CGT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC CCC AAT Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn 500 505 510			2012
GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT TGG CTG Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu 515 520 525 530			2060
CCC AAT CCC AAC CTG AAA GCC GAG CGC ACG ACC ACC CAC ACC CTC TCT Pro Asn Pro Asn Leu Lys Ala Glu Arg Thr Thr His Thr Leu Ser 535 540 545			2108
CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG TAT CAA Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln 550 555 560			2156
AGC AAT TAC CGC AAT TTC CTG TCT GAA GAG CAG AAG CTG ACC ACC AGC Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser 565 570 575			2204
GGC GAT GTC AGC TGT ACT CAG ATG AAT TAC TAC TAC GGT ATG TGT AGC Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Gly Met Cys Ser 580 585 590			2252
AAT CCT TAT TCC GAA AAA CTG GAA TGG CAG ATG CAA AAT ATC GAC AAG Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile Asp Lys 595 600 605 610			2300
GCC AGA ATC CGC GGT ATC GAG CTG ACG GGC CGT CTG AAT GTG GAC AAA Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp Lys 615 620 625			2348

B1
cont

GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA CTG TTC GGC TCG CTG GGT	2396
Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly	
630 635 640	
TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TTC ACC CAG	2444
Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Phe Thr Gln	
645 650 655	
CCG TTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA AAA	2492
Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys	
660 665 670	
TGG GGC GTG TTC TCC CGC CTG ACC TAT CTG GGC GCG AAA AAG GTC AAA	2540
Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys	
675 680 685 690	
GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT TTG	2588
Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro Leu	
695 700 705	
CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG	2636
Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val	
710 715 720	
TTC GAT ATG TAC GGC TTC TAC AAA CCG GTG AAA AAC CTG ACT TTG CGT	2684
Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr Leu Arg	
725 730 735	
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC	2732
Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser	
740 745 750	
CTG CGC GGC CTG TAT AGC TAC AGC ACC ACC AAC TCG GTC GAC CGC GAT	2780
Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp Arg Asp	
755 760 765 770	
GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA AGC CGT AAT TAC GCC GTA	2828
Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr Ala Val	
775 780 785	
TCG CTG GAA TGG AAG TTT TA ATCTGGTATT ATTGAATTAA TCGCCTTGTT	2878
Ser Leu Glu Trp Lys Phe	
790	
GAAAATTAAA GCCGTCCGAA TTGTGTTCAA GAACTCATTC GGACGGTTTT TACCGAATCT	2938
GTGTGTGGGT TTATAGTGGA TTAACAAAAA TCAGGACAAG GCGACGAAGC CGCAGACAGT	2998
ACAGATAGTA CGGAACCGAT TCACTTGGTG AGACCTTGC AAAATTCCCT TCCCTCCCGA	3058
CAGCCGAAAC CCAAACACAG GTTTCGGCT GTTTCGCCC CAAATACCTC CTAATTCTAC	3118
CCAAATACCC CCTTAATCCT CCCCCGATACC CGATAATCAG GCATCCGGCG CCTTTAGGCG	3178
GCAGCGGGCG CACTAACCT GTTGGCGGCT TTCAAAAGGT TCAAACACAT CGCCTTCAGG	3238
TGCCTTGCG CACTCACTTT AATCAGTCCG AAATAGGCCG CCCGCGCATA GCAGAACTTA	3298

31
cont.

CGGTGCAGCG TACCGAAGCT T

3319

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Val Lys Ala Val Arg Gly Lys Gly Gln Arg Asn
35 40 45

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240

B1
CONT

Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
260 265 270

Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
275 280 285

Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu
305 310 315 320

Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala
325 330 335

Val Asn Tyr Lys Gly Ser Phe Pro Ile Glu Asp Ser Ser Thr Leu Thr
340 345 350

Arg Asn Tyr Asn Gln Lys Asp Leu Asp Glu Ile Tyr Asn Arg Ser Met
355 360 365

Asp Thr Arg Phe Lys Arg Ile Thr Leu Arg Leu Asp Ser His Pro Leu
370 375 380

Gln Leu Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser
385 390 395 400

Arg Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly
405 410 415

Arg Val Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr
420 425 430

Asn Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe
435 440 445

Ser Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln
450 455 460

Glu Leu Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala
465 470 475 480

Asn Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu
485 490 495

Asn Gln Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val
500 505 510

Pro Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn
515 520 525

Trp Leu Pro Asn Pro Asn Leu Lys Ala Glu Arg Thr Thr His Thr
530 535 540

Leu Ser Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu
545 550 555 560

B
Cmt.

Tyr Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr
565 570 575

Thr Ser Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met
580 585 590

Cys Ser Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile
595 600 605

Asp Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val
610 615 620

Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser
625 630 635 640

Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Phe
645 650 655

Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser
660 665 670

Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys
675 680 685

Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr
690 695 700

Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala
705 710 715 720

Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr
725 730 735

Leu Arg Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp
740 745 750

Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp
755 760 765

Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr
770 775 780

Ala Val Ser Leu Glu Trp Lys Phe
785 790

B
Cont.
(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAA CCA TTA CAA ATG CCC CCT ATC GCC GCG CTG CTC GGC AGT ATT	48
Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile	
1 5 10 15	
TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA	96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGT CAG CGC AAT	144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn	
35 40 45	
GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA	192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu	
50 55 60	
ATG ATA CGC GAC AAT AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC	240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
TTG AGC GAC AGG AGC CGT CAT CAA AAA GGC TTT GCC ATT CGC GGC GTG	288
Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val	
85 90 95	
GAA GGC GAC CGT GTC GGC GTT AGT ATT GAC GGC GTA AAC CTG CCT GAT	336
Glu Gly Asp Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp	
100 105 110	
TCC GAA GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG	384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	
115 120 125	
CGT CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC ATC GTA AAA	432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys	
130 135 140	
GGG GCG GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG	480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val	
145 150 155 160	
AAT TAC CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG	528
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln	
165 170 175	
TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG	576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	
180 185 190	
ACA AAT ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT	624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala	
195 200 205	
TTG CTG TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAG	672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys	
210 215 220	

B1
Cont.

CGT GGT TAT CCG GTA GAG GGT GCT GGT AGC GGA GCG AAT ATC CGT GGT	720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly	
225 230 235 240	
TCT GCG CGC GGT ATT CCT GAT CCG TCC CAA CAC AAA TAC CAC AGC TTC	768
Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe	
245 250 255	
TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA	816
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala	
260 265 270	
TCG CTC AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC	864
Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr	
275 280 285	
AAC CTG CTT GCT TCT TAT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG	912
Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg	
290 295 300	
CGT AAC ACC AAC CTC TTT TAC GAA TGG ACG CCG GAA TCC GAC CGG TTG	960
Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu	
305 310 315 320	
TCT ATG GTA AAA GCG GAT GTC GAT TAT CAA AAA ACC AAA GTA TCT GCG	1008
Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala	
325 330 335	
GTC AAC TAC AAA GGT TCG TTC CCG ACG AAT TAC ACC ACA TGG GAA ACC	1056
Val Asn Tyr Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr	
340 345 350	
GAG TAC CAT AAA AAG GAA GTT GGC GAA ATC TAT AAC CGC AGC ATG GAT	1104
Glu Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp	
355 360 365	
ACA ACC TTC AAA CGT ATT ACG CTG CGT ATG GAC AGC CAT CCG TTG CAA	1152
Thr Thr Phe Lys Arg Ile Thr Leu Arg Met Asp Ser His Pro Leu Gln	
370 375 380	
CTC GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACC TTT GCC GGG CAG	1200
Leu Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Gly Gln	
385 390 395 400	
CGT GAT TTT GAA AAC TTA AAC CGC GAC GAT TAC TAC TTC AGC GGC CGT	1248
Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg	
405 410 415	
GTT GTT CGA ACC ACC AAC AGT ATC CAG CAT CCG GTG AAA ACC ACC AAC	1296
Val Val Arg Thr Thr Asn Ser Ile Gln His Pro Val Lys Thr Thr Asn	
420 425 430	
TAC GGT TTC TCG CTG TCC GAC CAA ATC CAA TGG AAC GAC GTG TTC AGT	1344
Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser	
435 440 445	
AGC CGC GCA GGT ATC CGT TAC GAC CAC ACC AAA ATG ACG CCT CAG GAA	1392
Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu	

3
cont

450	455	460	
TTG AAT GCC GAC TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAC Leu Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn 465 470 475 480			1440
ACT TAT AAA GGC TGG AGC GGA TTT GTC GGC TTG GCG GCG CAG CTG AGC Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Ser 485 490 495			1488
CAA ACA TGG CGT TTG GGT TAC GAT GTG ACC TCA GGT TTC CGC GTG CCG Gln Thr Trp Arg Leu Gly Tyr Asp Val Thr Ser Gly Phe Arg Val Pro 500 505 510			1536
AAT GCG TCT GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGC ACT TGG Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Thr Trp 515 520 525			1584
AAG CCT AAT CCT AAT TTG AAG GCA GAA CGC AGC ACC ACC CAC ACC CTG Lys Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu 530 535 540			1632
TCC TTG CAG GGG CGC GGC GAC AAA GGG ACA CTG GAT GCC AAC CTG TAT Ser Leu Gln Gly Arg Gly Asp Lys Gly Thr Leu Asp Ala Asn Leu Tyr 545 550 555 560			1680
CAA AGC AAT TAC CGA AAC TTC CTG TCG GAA GAG CAG AAT CTG ACT GTC Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Val 565 570 575			1728
AGC GGC ACA CCC GGC TGT ACT GAG GAG GAT GCT TAC TAC TAT AGA TGC Ser Gly Thr Pro Gly Cys Thr Glu Glu Asp Ala Tyr Tyr Arg Cys 580 585 590			1776
AGC GAC CCC TAC AAA GAA AAA CTG GAT TGG CAG ATG AAA AAT ATC GAC Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp 595 600 605			1824
AAG GCC AGA ATC CGC GGT ATC GAG TTG ACA GGC CGT CTG AAT GTG GAC Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp 610 615 620			1872
AAA GTA GCG TCT TTT GTT CCT GAG GGT TGG AAA CTG TTC GGC TCG CTG Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu 625 630 635 640			1920
GGT TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACA Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr 645 650 655			1968
CAG CCG CTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu 660 665 670			2016
AAA TGG GGC GTA TTC TCC CGC CTG ACC TAT CTA GGC GCG AAA AAG GTC Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val 675 680 685			2064

B1
cont

AAA GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro 690 695 700	2112
TTG CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr 705 710 715 720	2160
GTG TTT GAT ATG TAC GGC TTC TAC AAA CCG GCT AAA AAC CTG ACT TTG Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu 725 730 735	2208
CGT GCA GGC GTG TAC AAC CTG TTC AAC CGC AAA TAC ACC ACT TGG GAT Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp 740 745 750	2256
TCC CTG CGC GGT TTA TAT AGC TAC AGC ACC ACC AAT GCG GTC GAC CGC Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg 755 760 765	2304
GAT GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA GGC CGC AAT TAC GCC Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala 770 775 780	2352
GTA TCG CTG GAA TGG AAG TTT TAA Val Ser Leu Glu Trp Lys Phe 785 790	2376

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 791 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

*B1
Cont*

Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile 1 5 10 15
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr 20 25 30
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn 35 40 45
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu 50 55 60
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly 65 70 75 80
Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val

85

90

95

Glu Gly Asp Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240

Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
260 265 270

Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
275 280 285

Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu
305 310 315 320

Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala
325 330 335

Val Asn Tyr Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr
340 345 350

Glu Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp
355 360 365

Thr Thr Phe Lys Arg Ile Thr Leu Arg Met Asp Ser His Pro Leu Gln
370 375 380

Leu Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Gly Gln
385 390 395 400

31
cont.

Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg
405 410 415

Val Val Arg Thr Thr Asn Ser Ile Gln His Pro Val Lys Thr Thr Asn
420 425 430

Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser
435 440 445

Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu
450 455 460

Leu Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn
465 470 475 480

Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Ser
485 490 495

Gln Thr Trp Arg Leu Gly Tyr Asp Val Thr Ser Gly Phe Arg Val Pro
500 505 510

Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Thr Trp
515 520 525

Lys Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu
530 535 540

Ser Leu Gln Gly Arg Gly Asp Lys Gly Thr Leu Asp Ala Asn Leu Tyr
545 550 555 560

Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Val
565 570 575

Ser Gly Thr Pro Gly Cys Thr Glu Glu Asp Ala Tyr Tyr Arg Cys
580 585 590

Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp
595 600 605

Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp
610 615 620

Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu
625 630 635 640

Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr
645 650 655

Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu
660 665 670

Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val
675 680 685

Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro
690 695 700

Lys Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr
705 710 715 720

B1
cont.

Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu
725 730 735

Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp
740 745 750

Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg
755 760 765

Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala
770 775 780

Val Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AAA CCA TTA CAA ATG CTC CCT ATC GCC GCG CTG GTC GGC AGT ATT 48
Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA 96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGC CAG CGC AAT 144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45

B
cont.

GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA 192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

ATG ATA CGC GAC AAC AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC 240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

TTG AGC GAC AGC GGC CGC CAT CAA AAA GGC TTT GCC GTT CGC GGC GTG 288
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

GAA GGC AAC CGT GTC GGC GTG AGC ATA GAC GGC GTA AAC CTG CCT GAT 336
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

TCC GAA GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG	384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	
115 120 125	
CGT CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAG ATC GTA AAA	432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Val Lys	
130 135 140	
GGG GCG GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG	480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val	
145 150 155 160	
AAT TAC CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG GAT GAC CGG CAG	528
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Asp Asp Arg Gln	
165 170 175	
TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG	576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	
180 185 190	
ACA AAT ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT	624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala	
195 200 205	
TTG CTG TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAC	672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Asn	
210 215 220	
CGT GGT TAT CCG GTA GAG GGT GCT GGT AAA GAA ACT AAT ATC CGT GGT	720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Lys Glu Thr Asn Ile Arg Gly	
225 230 235 240	
TCT GCG CGC GGT ATT CCT GAT CCG TCC AAA CAC AAA TAC CAC AAC TTC	768
Ser Ala Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe	
245 250 255	
TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA	816
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala	
260 265 270	
TCG CTC AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC	864
Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Ser Tyr	
275 280 285	
AAC CTG ACT GCT TCT TCT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG	912
Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg	
290 295 300	
CGT AAC GCT AAC CTC TTT TAC GAA TGG ATG CCG GAT TCC AAC TGG TTG	960
Arg Asn Ala Asn Leu Phe Tyr Glu Trp Met Pro Asp Ser Asn Trp Leu	
305 310 315 320	
TCT TCT CTC AAA GCG GAT TTC GAT TAT CAA AAA ACC AAA GTA GCT GCG	1008
Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Lys Thr Lys Val Ala Ala	
325 330 335	
ATC AAC AAA GGT TCG TTC CCG ACT AAC TAT ACC ACC TGG GAA ACC GAA	1056
Ile Asn Lys Gly Ser Phe Pro Thr Asn Tyr Thr Trp Glu Thr Glu	

B
cont.

340	345	350	
TAC CAT CAA AAG GAA GTT GGT GAA ATC TAC AAC CGC AGT ATG GAT ACC Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp Thr 355 360 365			1104
CGC TTC AAA CGT TTT ACG CTG CGT TTG GAC AGC CAT CCG TTG CAA CTC Arg Phe Lys Arg Phe Thr Leu Arg Leu Asp Ser His Pro Leu Gln Leu 370 375 380			1152
GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACT TTC GCC AGC CGC CGT Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser Arg Arg 385 390 395 400			1200
GAT TTT GAA AAC CTA AAC CGC GAC TAT TAC TAC TTC AGC GGC CGT GTT Asp Phe Glu Asn Leu Asn Arg Asp Tyr Tyr Phe Ser Gly Arg Val 405 410 415			1248
GTT CGA ACC ACC AGC AGT ATC CAG CAT CCG GTG AAA ACC ACC AAC TAC Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr 420 425 430			1296
GGT TTC TCA CTG TCT GAC CAA ATT CAA TGG AAC GAC GTG TTC AGT AGC Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser 435 440 445			1344
CGC GCA GGT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG GAA TTG Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu 450 455 460			1392
AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAC ACT Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr 465 470 475 480			1440
TAT AAA GGC TGG AGC GGT TTT GTC GGC TTG GCG GCG CAA CTG AAT CAG Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln 485 490 495			1488
GCT TGG CGT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC CCC AAT Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn 500 505 510			1536
GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT TGG CTG Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu 515 520 525			1584
CCC AAT CCC AAC CTG AAA GCC GAG CGC TCG ACC ACC CAC ACC CTC TCT Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser 530 535 540			1632
CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG TAT CAA Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln 545 550 555 560			1680
AGC AAT TAC CGA AAT TTC CTG TCT GAA GAG CAG AAG CTG ACC ACC AGC Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser 565 570 575			1728

B
Cmt

GGC ACT CCC GGC TGT ACT GAG GAG AAT GCC TAC TAC TCT ATC TGT AGC Gly Thr Pro Gly Cys Thr Glu Glu Asn Ala Tyr Tyr Ser Ile Cys Ser 580 585 590	1776
GAC CCT TAT AAG GAA AAA CTG GAA TGG CAG ATG CAA AAT ATC GAC AAG Asp Pro Tyr Lys Glu Lys Leu Glu Trp Gln Met Gln Asn Ile Asp Lys 595 600 605	1824
GCC AGA ATC CGC GGT ATC GAG CTG ACG GGC CGT CTG AAT GTG GAC AAA Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp Lys 610 615 620	1872
GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA CTG TTC GGC TCG CTG GGT Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly 625 630 635 640	1920
TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACC CAG Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln 645 650 655	1968
CCG TTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA AAA Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys 660 665 670	2016
TGG GGC GTG TTC TCC CGC CTG ACC TAT CTG GGC GCG AAA AAG GTC AAA Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys 675 680 685	2064
GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT TTG Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro Leu 690 695 700	2112
CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val 705 710 715 720	2160
TTC GAT ATG TAC GGC TTC TAC AAA CCG GTG AAA AAC CTG ACT TTG CGT Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr Leu Arg 725 730 735	2208
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser 740 745 750	2256
CTG CGC GGC CTG TAT AGC TAC AGC ACC ACC AAC TCG GTC GAC CGC GAT Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp Arg Asp 755 760 765	2304
GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA GGC CGT AAT TAC GCC GTA Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala Val 770 775 780	2352
TCG CTG GAA TGG AAG TTT TAA Ser Leu Glu Trp Lys Phe 785 790	2379

B1
cont.

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Val Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Asp Asp Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Asn
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Lys Glu Thr Asn Ile Arg Gly
225 230 235 240

Ser Ala Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe
245 250 255

*31
cont.*

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
260 265 270

Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
275 280 285

Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Ala Asn Leu Phe Tyr Glu Trp Met Pro Asp Ser Asn Trp Leu
305 310 315 320

Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Lys Thr Lys Val Ala Ala
325 330 335

Ile Asn Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr Glu
340 345 350

Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp Thr
355 360 365

Arg Phe Lys Arg Phe Thr Leu Arg Leu Asp Ser His Pro Leu Gln Leu
370 375 380

Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser Arg Arg
385 390 395 400

Asp Phe Glu Asn Leu Asn Arg Asp Tyr Tyr Tyr Phe Ser Gly Arg Val
405 410 415

Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr
420 425 430

Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser
435 440 445

Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu
450 455 460

Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Gln
465 470 475 480

Asn Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu
485 490 495

Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn
500 505 510

Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu
515 520 525

Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser
530 535 540

Leu Gln Gly Arg Ser Glu Lys Gly Met Leu Asp Ala Asn Leu Tyr Gln
545 550 555 560

Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser
565 570 575

31
cont.

Gly Thr Pro Gly Cys Thr Glu Glu Asn Ala Tyr Tyr Ser Ile Cys Ser
580 585 590

Asp Pro Tyr Lys Glu Lys Leu Glu Trp Gln Met Lys Asn Ile Asp Lys
595 600 605

Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp Lys
610 615 620

Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly
625 630 635 640

Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln
645 650 655

Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys
660 665 670

Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys
675 680 685

Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro Leu
690 695 700

Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val
705 710 715 720

Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr Leu Arg
725 730 735

Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser
740 745 750

Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg Asp
755 760 765

Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala Val
770 775 780

Ser Leu Glu Trp Lys Phe
785 790

B1
cont
(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG AAA CCA TTA CAC ATG CTT CCT ATT GCC GCG CTG GTC GGC AGT ATT	48
Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile	
1 5 10 15	
TTC GGC AAT CCG GTC TTG GCA GCG GAT GAA GCT GCA ACC GAA ACC ACA	96
Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
CCC GTT AAA GCA GAG ATA AAA GAA GTG CGC GTT AAA GAC CAG CTT AAT	144
Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn	
35 40 45	
GCG CCT GCA ACC GTG GAA CGT GTC AAC CTC GGC CGC ATT CAA CAG GAA	192
Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu	
50 55 60	
ATG ATA CGC GAC AAC AAA GAC TTG GTG CGT TAC TCC ACC GAC GTC GGC	240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
TTG AGC GAT AGC GGC CGC CAT CAA AAA GGC TTT GCT GTG CGC GGC GTG	288
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val	
85 90 95	
GAA GGC AAC CGT GTC GGT GTC AGC ATT GAC GGC GTG AGC CTG CCT GAT	336
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp	
100 105 110	
TCG GAA GAA AAC TCA CTG TAT GCA CGT TAT GGC AAC TTC AAC AGC TCG	384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	
115 120 125	
CGC CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAA ATC GCG AAG	432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys	
130 135 140	
GGC GCT GAC TCT TTC AAT ACC GGT AGC GGC GCA TTG GGT GGC GGC GTG	480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val	
145 150 155 160	
AAT TAC CAA ACC CTG CAA GGA CAT GAT TTG CTG TTG GAC GAC AGG CAA	528
Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Leu Asp Asp Arg Gln	
165 170 175	
TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGC AAC CGC GAA TGG	576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	
180 185 190	
ACA AAT ACA CTC GGT TTC GGT GTG AGC AAC GAC CGC GTG GAT GCC GCT	624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala	
195 200 205	
TTG CTG TAT TCG CAA CGT CGC GGT CAT GAG ACC GAA AGC GCG GGC GAG	672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu	
210 215 220	
CGT GGC TAT CCG GTA GAG GGT GCT GGC AGC GGA GCA ATT ATC CGT GGT	720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Ile Ile Arg Gly	
225 230 235 240	

B
Cont

TCG TCA CGC GGT ATC CCT GAT CCG TCC AAA CAC AAA TAC CAC AAC TTC Ser Ser Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe 245 250 255	768
TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAG CAC CGC ATC GGC CCA Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Lys His Arg Ile Gly Pro 260 265 270	816
TCG TTT AAC GGC CAG CAG GGG CAT AAT TAC ACG ATT GAA GAG TCT TAT Ser Phe Asn Gly Gln Gln Gly His Asn Tyr Thr Ile Glu Glu Ser Tyr 275 280 285	864
AAC CTG ACC GCT TCT TCC TGG CGC GAA GCC GAT GAC GTA AAC AGA CGG Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg 290 295 300	912
CGC AAT GCC AAC CTC TTT TAC GAA TGG ACG CCT GAT TCA AAT TGG CTG Arg Asn Ala Asn Leu Phe Tyr Glu Trp Thr Pro Asp Ser Asn Trp Leu 305 310 315 320	960
TCG TCT TTG AAG GCG GAT TTC GAT TAT CAG ACA ACC AAA GTG GCG GCG Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Thr Thr Lys Val Ala Ala 325 330 335	1008
GTT AAC AAC AAA GGC TCG TTC CCG ACG GAT TAT TCC ACC TTG ACG CGC Val Asn Asn Lys Gly Ser Phe Pro Thr Asp Tyr Ser Thr Leu Thr Arg 340 345 350	1056
AAC TAT AAT CAG AAG GAT TTG GAG AAT ATA TAC AAC CGC AGC ATG GAC Asn Tyr Asn Gln Lys Asp Leu Glu Asn Ile Tyr Asn Arg Ser Met Asp 355 360 365	1104
ACC CGA TTC AAA CGT TTT ACT TTG CGT ATG GAC AGC CAA CCG TTG CAA Thr Arg Phe Lys Arg Phe Thr Leu Arg Met Asp Ser Gln Pro Leu Gln 370 375 380	1152
CTG GGC GGC CAA CAT CGC TTG TCG CTT AAA ACT TTC GCC AGT CGG CGT Leu Gly Gly Gln His Arg Leu Ser Leu Lys Thr Phe Ala Ser Arg Arg 385 390 395 400	1200
GAG TTT GAA AAC TTA AAC CGC GAC GAT TAT TAC TTC AGC GAA AGA GTA Glu Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Glu Arg Val 405 410 415	1248
TCC CGT ACT ACC AGC TCG ATT CAA CAC CCC GTG AAA ACC ACT AAT TAT Ser Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr 420 425 430	1296
GGT TTC TCA CTG TCT GAT CAA ATC CAA TGG AAC GAC GTG TTC AGC AGC Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser 435 440 445	1344
CGT GCA GAT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG GAA TTG Arg Ala Asp Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu 450 455 460	1392
AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAT ACT Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr	1440

B1
Cont

465	470	475	480	
TAT AAA GGC TGG AGC GGA TTT GTC GGT TTG GCG GCG CAA CTG AAT CAG				1488
Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln				
485	490	495		
GCT TGG CAT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC CCC AAT				1536
Ala Trp His Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn				
500	505	510		
GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT TGG CTG				1584
Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu				
515	520	525		
CCC AAT CCC AAC CTG AAA GCC GAG CGC AGC ACC ACC CAC ACC CTG TCT				1632
Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser				
530	535	540		
CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG TAT CAA				1680
Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln				
545	550	555	560	
AGC AAT TAC CGA AAC TTC TTG TCT GAA GAG CAG AAG CTG ACC ACC AGC				1728
Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser				
565	570	575		
GGC GAT GTC GGC TGT ACT CAG ATG AAT TAC TAC TAC GGT ATG TGT AGC				1776
Gly Asp Val Gly Cys Thr Gln Met Asn Tyr Tyr Gly Met Cys Ser				
580	585	590		
AAT CCT TAT TCC GAA AAA CCG GAA TGG CAG ATG CAA AAT ATC GAT AAG				1824
Asn Pro Tyr Ser Glu Lys Pro Glu Trp Gln Met Gln Asn Ile Asp Lys				
595	600	605		
GCC CGA ATC CGT GGT CTT GAG CTG ACG GGC CGT CTG AAT GTG ACA AAA				1872
Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val Thr Lys				
610	615	620		
GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA TTG TTC GGC TCG CTG GGT				1920
Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly				
625	630	635	640	
TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACA CAG				1968
Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln				
645	650	655		
CCG CCG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA AAA				2016
Pro Pro Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys				
660	665	670		
TGG GGT GTG TTC TCC CGC CTG ACT TAT CTG GGT GCG AAA AAG GTC AAA				2064
Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys				
675	680	685		
GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC CGG GGT ACG CCT TTG				2112
Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu				
690	695	700		

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Cont

CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val 705 710 715 720	2160
TTT GAT ATG TAC GGC TTC TAC AAA CTG GCT AAA AAC CTG ACT TTG CGT Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg 725 730 735	2208
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser 740 745 750	2256
CTG CGC GGT TTG TAT AGC TAC ACC ACC AAC GCG GTC GAC CGA GAT Leu Arg Gly Leu Tyr Ser Tyr Thr Thr Asn Ala Val Asp Arg Asp 755 760 765	2304
GGC AAA GGC TTA GAC CGC TAC CGC GCC TCA GGC CGT AAT TAC GCC GTA Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val 770 775 780	2352
TCG CTG GAT TGG AAG TTT TGAATTCC Ser Leu Asp Trp Lys Phe 885 790	2378

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn
35 40 45

Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser

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cont*

115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Leu Asp Asp Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Ile Ile Arg Gly
225 230 235 240

Ser Ser Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Lys His Arg Ile Gly Pro
260 265 270

Ser Phe Asn Gly Gln Gln Gly His Asn Tyr Thr Ile Glu Glu Ser Tyr
275 280 285

Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Ala Asn Leu Phe Tyr Glu Trp Thr Pro Asp Ser Asn Trp Leu
305 310 315 320

Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Thr Thr Lys Val Ala Ala
325 330 335

Val Asn Asn Lys Gly Ser Phe Pro Thr Asp Tyr Ser Thr Leu Thr Arg
340 345 350

Asn Tyr Asn Gln Lys Asp Leu Glu Asn Ile Tyr Asn Arg Ser Met Asp
355 360 365

Thr Arg Phe Lys Arg Phe Thr Leu Arg Met Asp Ser Gln Pro Leu Gln
370 375 380

Leu Gly Gly Gln His Arg Leu Ser Leu Lys Thr Phe Ala Ser Arg Arg
385 390 395 400

Glu Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Glu Arg Val
405 410 415

Ser Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr
420 425 430

B1
cont

Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser
435 440 445

Arg Ala Asp Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu
450 455 460

Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr
465 470 475 480

Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln
485 490 495

Ala Trp His Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn
500 505 510

Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu
515 520 525

Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser
530 535 540

Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln
545 550 555 560

Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser
565 570 575

Gly Asp Val Gly Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met Cys Ser
580 585 590

Asn Pro Tyr Ser Glu Lys Pro Glu Trp Gln Met Gln Asn Ile Asp Lys
595 600 605

Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val Thr Lys
610 615 620

Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly
625 630 635 640

Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln
645 650 655

Pro Pro Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys
660 665 670

Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys
675 680 685

Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu
690 695 700

Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val
705 710 715 720

Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg
725 730 735

Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser
740 745 750

B
cont

Leu Arg Gly Leu Tyr Ser Tyr Thr Thr Thr Asn Ala Val Asp Arg Asp
755 760 765

Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val
770 775 780

Ser Leu Asp Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gln Gln Gln His Leu Phe Arg Leu Asn Ile Leu Cys Leu Ser Leu
1 5 10 15

Met Thr Ala Leu Pro Val Tyr Ala Glu Asn Val Gln Ala Glu Gln Ala
20 25 30

Gln Glu Lys Gln Leu Asp Thr Ile Val Lys Ala Lys Lys Gln Lys Thr
35 40 45

Arg Arg Asp Asn Glu Val Thr Gly Leu Gly Lys Leu Val Lys Ser Ser
50 55 60

Asp Thr Leu Ser Lys Glu Gln Val Leu Asn Ile Arg Asp Leu Thr Arg
65 70 75 80

Tyr Asp Pro Gly Ile Ala Val Val Glu Gln Gly Arg Gly Ala Ser Ser
85 90 95

Gly Tyr Ser Ile Arg Gly Met Asp Lys Asn Arg Val Ser Leu Thr Val
100 105 110

Asp Gly Val Ser Gln Ile Gln Ser Tyr Thr Ala Gln Ala Ala Leu Gly
115 120 125

Gly Thr Arg Thr Ala Gly Ser Ser Gly Ala Ile Asn Glu Ile Glu Tyr
130 135 140

Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Ser Asn Ser Ser Glu
145 150 155 160

Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Ala Phe Gln Thr Lys Thr
165 170 175

Ala Ala Asp Ile Ile Gly Glu Gly Lys Gln Trp Gly Ile Gln Ser Lys
180 185 190

Thr Ala Tyr Ser Gly Lys Asp His Ala Leu Thr Gln Ser Leu Ala Leu
195 200 205

B1
Cont

Ala Gly Arg Ser Gly Gly Ala Glu Ala Leu Leu Ile Tyr Thr Lys Arg
210 215 220

Arg Gly Arg Glu Ile His Ala His Lys Asp Ala Gly Lys Gly Val Gln
225 230 235 240

Ser Phe Asn Arg Leu Pro Ile Cys Arg Phe Gly Asn Asn Thr Tyr Thr
245 250 255

Asp Cys Thr Pro Arg Asn Ile Gly Gly Asn Gly Tyr Tyr Ala Ala Val
260 265 270

Gln Asp Asn Val Arg Leu Gly Arg Trp Ala Asp Val Gly Ala Gly Ile
275 280 285

Arg Tyr Asp Tyr Arg Ser Thr His Ser Glu Asp Lys Ser Val Ser Thr
290 295 300

Gly Thr His Arg Asn Leu Ser Trp Asn Ala Gly Val Val Leu Lys Pro
305 310 315 320

Phe Thr Trp Met Asp Leu Thr Tyr Arg Ala Ser Thr Gly Phe Arg Leu
325 330 335

Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Ala Gly Glu Ser Leu Lys
340 345 350

Thr Leu Asp Leu Lys Pro Glu Lys Ser Phe Asn Arg Glu Ala Gly Ile
355 360 365

Val Phe Lys Gly Asp Phe Gly Asn Leu Glu Ala Ser Tyr Phe Asn Asn
370 375 380

Ala Tyr Arg Asp Leu Ile Ala Phe Gly Tyr Glu Thr Arg Thr Gln Asn
385 390 395 400

Gly Gln Thr Ser Ala Ser Gly Asp Pro Gly Tyr Arg Asn Ala Gln Asn
405 410 415

Ala Arg Ile Ala Gly Ile Asn Ile Leu Gly Lys Ile Asp Trp His Gly
420 425 430

Val Trp Gly Gly Leu Pro Asp Gly Leu Tyr Ser Thr Leu Ala Tyr Asn
435 440 445

Arg Ile Lys Val Lys Asp Ala Asp Arg Ala Asp Arg Thr Phe Val Thr
450 455 460

Ser Tyr Leu Phe Asp Ala Val Gln Pro Ser Arg Tyr Val Leu Gly Leu
465 470 475 480

Gly Tyr Asp His Pro Asp Gly Ile Trp Gly Ile Asn Thr Met Phe Thr
485 490 495

Tyr Ser Lys Ala Lys Ser Val Asp Glu Leu Leu Gly Ser Gln Ala Leu
500 505 510

Leu Asn Gly Asn Ala Asn Ala Lys Lys Ala Ala Ser Arg Arg Thr Arg
515 520 525

31
cont

Pro Trp Tyr Val Thr Asp Val Ser Gly Tyr Tyr Asn Ile Lys Lys His
530 535 540

Leu Thr Leu Arg Ala Gly Val Tyr Asn Leu Leu Asn Tyr Arg Tyr Val
545 550 555 560

Thr Trp Glu Asn Val Arg Gln Thr Ala Gly Gly Ala Val Asn Gln His
565 570 575

Lys Asn Val Gly Val Tyr Asn Arg Tyr Ala Ala Pro Gly Arg Asn Tyr
580 585 590

Thr Phe Ser Leu Glu Met Lys Phe
595 600

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Lys Lys His Gly Phe Gln Leu Thr Leu Thr Ala Leu Ala Val
1 5 10 15

Ala Ala Ala Phe Pro Ser Tyr Ala Ala Asn Pro Glu Thr Ala Ala Pro
20 25 30

Asp Ala Ala Gln Thr Gln Ser Leu Lys Glu Val Thr Val Arg Ala Ala
35 40 45

Lys Val Gly Arg Arg Ser Lys Glu Ala Thr Gly Leu Gly Lys Ile Ala
50 55 60

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cont

Lys Thr Ser Glu Thr Leu Asn Lys Glu Gln Val Leu Gly Ile Arg Asp
65 70 75 80

Leu Thr Arg Tyr Asp Pro Gly Val Ala Val Val Glu Gln Gly Asn Gly
85 90 95

Ala Ser Gly Glu Tyr Ser Ile Arg Gly Val Asp Lys Asn Arg Val Ala
100 105 110

Val Ser Val Asp Gly Val Ala Gln Ile Gln Ala Phe Thr Val Gln Gly
115 120 125

Ser Leu Ser Gly Tyr Gly Gly Arg Gly Ser Gly Ala Ile Asn Glu
130 135 140

Ile Glu Tyr Glu Asn Ile Ser Thr Val Glu Ile Asp Lys Gly Ala Gly
145 150 155 160

Ser Ser Asp His Gly Ser Gly Ala Leu Gly Gly Ala Val Ala Phe Arg
165 170 175

Thr Lys Glu Ala Ala Asp Leu Ile Ser Asp Gly Lys Ser Trp Gly Ile
180 185 190

Gln Ala Lys Thr Ala Tyr Gly Ser Lys Asn Arg Gln Phe Met Lys Ser
195 200 205

Leu Gly Ala Gly Phe Ser Lys Asp Gly Trp Glu Gly Leu Leu Ile Arg
210 215 220

Thr Glu Arg Gln Gly Arg Glu Thr His Pro His Gly Asp Ile Ala Asp
225 230 235 240

Gly Val Ala Tyr Gly Ile Asn Arg Leu Ser Val Cys Gly Tyr Ile Glu
245 250 255

Thr Leu Arg Ser Arg Lys Cys Val Pro Arg Lys Ile Asn Gly Ser Asn
260 265 270

Ile His Ile Ser Leu Asn Asp Arg Phe Ser Ile Gly Lys Tyr Phe Asp
275 280 285

Phe Ser Leu Gly Gly Arg Tyr Asp Arg Lys Asn Phe Thr Thr Ser Glu
290 295 300

Glu Leu Val Arg Ser Gly Arg Tyr Val Asp Arg Ser Trp Asn Ser Gly
305 310 315 320

Ile Val Phe Lys Pro Asn Arg His Phe Ser Leu Ser Tyr Arg Ala Ser
325 330 335

Ser Gly Phe Arg Thr Pro Ser Phe Gln Glu Leu Phe Gly Ile Asp Ile
340 345 350

Tyr His Asp Tyr Pro Lys Gly Trp Gln Arg Pro Ala Leu Lys Ser Glu
355 360 365

Lys Ala Ala Asn Arg Glu Ile Gly Leu Gln Trp Lys Gly Asp Phe Gly
370 375 380

Phe Leu Glu Ile Ser Ser Phe Arg Asn Arg Tyr Thr Asp Met Ile Ala
385 390 395 400

Val Ala Asp His Lys Thr Lys Leu Pro Asn Gln Ala Gly Gln Leu Thr
405 410 415

Glu Ile Asp Ile Arg Asp Tyr Tyr Asn Ala Gln Asn Met Ser Leu Gln
420 425 430

Gly Val Asn Ile Leu Gly Lys Ile Asp Trp Asn Gly Val Tyr Gly Lys
435 440 445

Leu Pro Glu Gly Leu Tyr Thr Thr Leu Ala Tyr Asn Arg Ile Lys Pro
450 455 460

Lys Ser Val Ser Asn Arg Pro Gly Leu Ser Leu Arg Ser Tyr Ala Leu
465 470 475 480

B
Cont.

Asp Ala Val Gln Pro Ser Arg Tyr Val Leu Gly Phe Gly Tyr Asp Gln
485 490 495

Pro Glu Gly Lys Trp Gly Ala Asn Ile Met Leu Thr Tyr Ser Lys Gly
500 505 510

Lys Asn Pro Asp Glu Leu Ala Tyr Leu Ala Gly Asp Gln Lys Arg Tyr
515 520 525

Ser Thr Lys Arg Ala Ser Ser Ser Trp Ser Thr Ala Asp Val Ser Ala
530 535 540

Tyr Leu Asn Leu Lys Lys Arg Leu Thr Leu Arg Ala Ala Ile Tyr Asn
545 550 555 560

Ile Gly Asn Tyr Arg Tyr Val Thr Trp Glu Ser Leu Arg Gln Thr Ala
565 570 575

Glu Ser Thr Ala Asn Arg His Gly Gly Asp Ser Asn Tyr Gly Arg Tyr
580 585 590

Ala Ala Pro Gly Arg Asn Phe Ser Leu Ala Leu Gly Met Lys Phe
595 600 605

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAACAGGTCT CGGCATAG

18

B1
Cont
(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGAATTCA AACAGGTCTC GGCATAG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGAATTCA AAAACTTCCA TTCCAGCGAT ACG

33

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAAAAACTTCC ATTCCAGCGA TACG

24

2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: peptide
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Thr Thr Pro Val Lys Ala
5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 792 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr

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Cont

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Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240

Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
260 265 270

Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
275 280 285

Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu
305 310 315 320

Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala
325 330 335

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Cont.

Val Asn Tyr Lys Gly Ser Phe Pro Ile Glu Asp Ser Ser Thr Leu Thr
340 345 350

Arg Asn Tyr Asn Gln Lys Asp Leu Asp Glu Ile Tyr Asn Arg Ser Met
355 360 365

Asp Thr Arg Phe Lys Arg Ile Thr Leu Arg Leu Asp Ser His Pro Leu
370 375 380

Gln Leu Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser
385 390 395 400

Arg Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly
405 410 415

Arg Val Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr
420 425 430

Asn Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe
435 440 445

Ser Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln
450 455 460

Glu Leu Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala
465 470 475 480

Asn Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu
485 490 495

Asn Gln Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val
500 505 510

Pro Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn
515 520 525

Trp Leu Pro Asn Pro Asn Leu Lys Ala Glu Arg Thr Thr Thr His Thr
530 535 540

Leu Ser Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu
545 550 555 560

Tyr Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr
565 570 575

Thr Ser Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Gly Met
580 585 590

Cys Ser Asn Pro Tyr Ser Glu Lys Leu Asp Trp Gln Met Gln Asn Ile
595 600 605

Asp Lys Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val
610 615 620

Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser
625 630 635 640

Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser

31
cont

645

650

655

Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser
660 665 670

Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys
675 680 685

Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr
690 695 700

Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala
705 710 715 720

Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr
725 730 735

Leu Arg Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp
740 745 750

Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp
755 760 765

Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr
770 775 780

Ala Val Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

B1
cont

Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val
85 90 95

Glu Gly Asp Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240

Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
260 265 270

Ser Leu Asn Gly Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
275 280 285

Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu
305 310 315 320

Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala
325 330 335

Val Asn Tyr Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr
340 345 350

Glu Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp
355 360 365

Thr Thr Phe Lys Arg Ile Thr Leu Arg Met Asp Ser His Pro Leu Gln
370 375 380

Leu Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Gly Gln

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Cont

385 390 395 400

Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg
405 410 415

Val Val Arg Thr Thr Asn Ser Ile Gln His Pro Val Lys Thr Thr Asn
420 425 430

Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser
435 440 445

Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu
450 455 460

Leu Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn
465 470 475 480

Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Ser
485 490 495

Gln Thr Trp Arg Val Gly Tyr Asp Val Thr Ser Gly Phe Arg Val Pro
500 505 510

Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Thr Trp
515 520 525

Lys Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu
530 535 540

Ser Leu Gln Gly Arg Gly Asp Lys Gly Thr Leu Asp Ala Asn Leu Tyr
545 550 555 560

Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Val
565 570 575

Ser Gly Thr Pro Gly Cys Thr Glu Glu Asp Ala Tyr Tyr Tyr Arg Cys
580 585 590

Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp
595 600 605

Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp
610 615 620

Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu
625 630 635 640

Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr
645 650 655

Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu
660 665 670

Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val
675 680 685

Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro
690 695 700

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Cont.*

Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr
705 710 715 720

Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu
725 730 735

Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp
740 745 750

Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg
755 760 765

Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala
770 775 780

Val Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Ile Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Val Lys
130 135 140

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Cont*

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Asp Asp Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Asn
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Lys Glu Thr Asn Ile Arg Gly
225 230 235 240

Ser Ala Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
260 265 270

Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
275 280 285

Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Ala Asn Leu Phe Tyr Glu Trp Met Pro Asp Ser Asn Trp Leu
305 310 315 320

Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Lys Thr Lys Val Ala Ala
325 330 335

Ile Asn Lys Gly Ser Phe Pro Thr Asn Tyr Thr Trp Glu Thr Glu
340 345 350

Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp Thr
355 360 365

Arg Phe Lys Arg Phe Thr Leu Arg Leu Asp Ser His Pro Leu Gln Leu
370 375 380

Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser Arg Arg
385 390 395 400

Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg Val
405 410 415

Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr
420 425 430

Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser
435 440 445

Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu
450 455 460

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cont*

Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr
465 470 475 480

Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln
485 490 495

Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn
500 505 510

Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu
515 520 525

Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser
530 535 540

Leu Gln Gly Arg Ser Glu Lys Gly Met Leu Asp Ala Asn Leu Tyr Gln
545 550 555 560

Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser
565 570 575

Gly Thr Pro Gly Cys Thr Glu Glu Asn Ala Tyr Tyr Ser Ile Cys Ser
580 585 590

Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp Lys
595 600 605

Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp Lys
610 615 620

Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly
625 630 635 640

Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln
645 650 655

Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys
660 665 670

Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys
675 680 685

Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro Leu
690 695 700

Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val
705 710 715 720

Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr Leu Arg
725 730 735

Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser
740 745 750

Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg Asp
755 760 765

Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala Val
770 775 780

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Cont

Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn
35 40 45

Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Asp Asp Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Ser Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu
210 215 220

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Cont

Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Ile Ile Arg Gly
225 230 235 240

Ser Ser Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Lys His Arg Ile Gly Pro
260 265 270

Ser Phe Asn Gly Gln Gln Gly His Asn Tyr Thr Ile Glu Glu Ser Tyr
275 280 285

Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Ala Asn Leu Phe Tyr Glu Trp Thr Pro Asp Ser Asn Trp Leu
305 310 315 320

Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Thr Thr Lys Val Ala Ala
325 330 335

Val Asn Asn Lys Gly Ser Phe Pro Thr Asp Tyr Ser Thr Trp Thr Arg
340 345 350

Asn Tyr Asn Gln Lys Asp Leu Glu Asn Ile Tyr Asn Arg Ser Met Asp
355 360 365

Thr Arg Phe Lys Arg Phe Thr Leu Arg Met Asp Ser Gln Pro Leu Gln
370 375 380

Leu Gly Gly Arg His Arg Leu Ser Leu Lys Thr Phe Ala Ser Arg Arg
385 390 395 400

Glu Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Glu Arg Val
405 410 415

Ser Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr
420 425 430

Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser
435 440 445

Arg Ala Asp Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu
450 455 460

Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr
465 470 475 480

Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln
485 490 495

Ala Trp His Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn
500 505 510

Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu
515 520 525

Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser
530 535 540

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Cont

Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln
545 550 555 560

Asn Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Thr Ser
565 570 575

Gly Asp Val Gly Cys Thr Gln Met Asn Tyr Tyr Gly Met Cys Ser
580 585 590

Asn Pro Tyr Ser Glu Lys Pro Glu Trp Gln Met Gln Asn Ile Asp Lys
595 600 605

Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val Thr Lys
610 615 620

Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly
625 630 635 640

Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln
645 650 655

Pro Pro Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys
660 665 670

Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Ala Lys
675 680 685

Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu
690 695 700

Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val
705 710 715 720

Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg
725 730 735

Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser
740 745 750

Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg Asp
755 760 765

Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val
770 775 780

Ser Leu Asp Trp Lys Phe
785 790

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